ENTHEOGENETICS
A GENETIC ENGINEERING PRIMER FOR THE VISION PLANTS: A NEW VISION FOR OUR TIME

We know that one of the main characteristics of the human species is a fascination with exploring alternative states of being and consciousness. The first roots of our human development, the shamanic cultures of our early human ancestors, already show a fascination with exploring alternative states of consciousness through ritual, sound, movement, ordeal, and entheogenic drug ingestion. These technologies of the sacred have been expanded over the centuries of human development in the disciplines of art, religion, sports, yoga, devotion, service, and the increasingly world-wide use of plant teachers. Recent research has lead many to postulate that all these technologies of ecstasy lead to the same petrochemical events(1).

These ancient and new ways of exploring alternative states of consciousness and connection have always appealed to a certain fraction of the earth's population, those who have an inquisitive mind and a daring nature. Now however, we are faced with the situation in which we have over five billion human beings on this planet, and a doubling time for our population of under forty years. We no longer have the luxury of unlimited time for a cultural elite to gradually evolve, and for cultural diffusion to gradually spread the ideas of this elite to our burgeoning population.

Accordingly, in this paper I will put forth the daring proposition that, along with the genetic engineering of our future population to meet environmental constraints, we also have the possibility of genetically engineering new, connected, mystical states of being, not just for the religious geniuses, or the mystically motivated, but for the common man and woman. It seems that only those states of mind that are common and ordinary among the population will have the ability to change the behavior patterns of our species in such fundamental ways so as to avoid an ecological catastrophe.

It is now possible to fully appreciate the implications of recombinant DNA technology and the psychedelic experience for the evolutionary future of our species. As one molecular geneticist has said, "It is possible to take a gene out of anything, and put it into anything".

The implications of this statement are that, as a species, we will theoretically be able to redesign any life forms we wish, including ourselves. From this point on, at least in theory, we can choose to be the inhabitants of any ecological niche we desire. As any successful species diversifies in order to fill ever more ecological niches, so we too have the possibility of re-acquiring the gills from the fish family in order to exploit the ocean depths, or to grow the coat of the bear in order to inhabit the northern climates without undue energy consumption. It is also possible to transform our annual food crops, the growing of which requires much labor, technology, and energy, into self-regenerating earth-healing perennials.

But it is to the genetic engineering of future states of consciousness of our species that I wish to address this paper.

We are currently socially fragmented and spiritually unconnected as a people. A handful in every generation experience the connected, aware states that our most highly developed people tell us are possible. These same highly developed people are the ones that innovate the social, legal and moral codes and forms for the rest of us.

But for the most part humanity is a disconnected group of people striving to maximize their own self interests. This results in social fragmentation, the drive to acquire more goods and better life styles as a hedge against the future, and an unsustainable assault against the earth's resources. As we fragment into nuclear families and attempt to insure our futures by everyone having children, the population grows uncontrollably. We are like cancer cells in a body, doing our own thing and maximizing our own growth.

There is a way out of this trap. It consists of humanity all being energetically and spiritually interconnected to each other in a very deep way, much as the great spiritual leaders of our past were connected. In this state we become more like the interconnected cells of the body, each doing the appropriate task to contribute to the success of the whole organism, and receiving satisfaction in doing so.

There are many ways to achieve these connected states, such as meditation, isolation, yoga, exertion, etc. The problem with all of them is that they require great motivation in order to perform them, which most people lack. Thus we must search for a method of evolving into a more connected human state that is applicable to all.

There is now a growing body of evidence from the study of South American ayahuasca shamanism that such states can be achieved at will in ordinary people by the ingestion of tryptamine and harmala alkaloids. In these shamanic cultures, people are connected energetically and socially in ways that seem to be very beneficial. Some experienced users of these substances report the formation of something like group consciousness.

The supplementation of these substances, which could be seen as a vitamins, could catalyze a very connected group-mind state in groups of people who would regularly use them. But here again, we run into the problem of motivation and opportunity. Not all will have both. And it is to all of humanity that we must be attentive. The future of our species must be an evolutionary one, that is, it must be made available to all by being part of our nature and being. Only then will it affect enough people to stop the out-of-control population and material growth.

This is where our new abilities in genetic engineering come in. We know the biosynthetic pathways that the plants use to synthesize visionary compounds, and we can move the genetic codes for the production of these compounds into any

organism we chose. So for example we could move them into *E. coli*, which has a symbiotic relationship with us in our gut. Modified *E. coli* strains could be introduced into our intestinal tract which would synthesize a steady flow of our deficient metabolites the absence of which causes us to be disconnected from each other.

Several recent studies have focused on the pineal gland and its role in mystical and spiritual experiences(2,3). The products of the pineal gland, which include the tryptamine alkaloid 5-methoxy-N,N-dimethyltryptamine (5-MEO-DMT)(4,5), are said to be released in large amounts during the birth experience, and thereafter decline during the early years, until during puberty, when the pineal gland partially calcifies and ceases production for most people. Many intriguing suppositions postulate that mystics and religious geniuses are those who have a biochemical disposition to sustained production of the tryptamine products from the pineal gland throughout life, and there is also interesting evidence that many of the spiritual practices are aimed at stimulating the production of this mysterious gland, located in the center of the forehead, the reputed spot of the third eye(6).

Supplementation with the product of this strangely quiescent master gland has been carried out in many cultures of our planet because of the use of shamanically sanctioned potions, such as ayahuasca(7). These shamanic potions contain DMT and 5-MeO DMT, along with an MAO inhibitor, in order to protect these active ingredients from being deactivated by protective body mechanisms in the digestive system. Studies seem to confirm that the regular use of potions containing these two tryptamines does not seem to be harmful, but on the contrary, they seem to endow their regular users with confidence, optimism, vigor and reflection, all characteristics that we would wish for in future generations(8,9).

In choosing to focus on the tryptamines, there is another and more practical reason to do so, and that is that they are produced by many plant families, and especially by a genus of grasses, the *Phalaris*, that is easy to grow and study and has a wide variability in genetic production of alkaloids, making it easy to manipulate.

Accordingly, the bulk of this paper will concentrate on presenting genetic information that may perhaps interest molecular biologists, geneticists, breeders, and others with an interest in psychological evolutionary biology.

GENETIC CONTROL OF PRODUCTION OF TRYPTAMINE FAMILIES IN PHALARIS SPECIES.

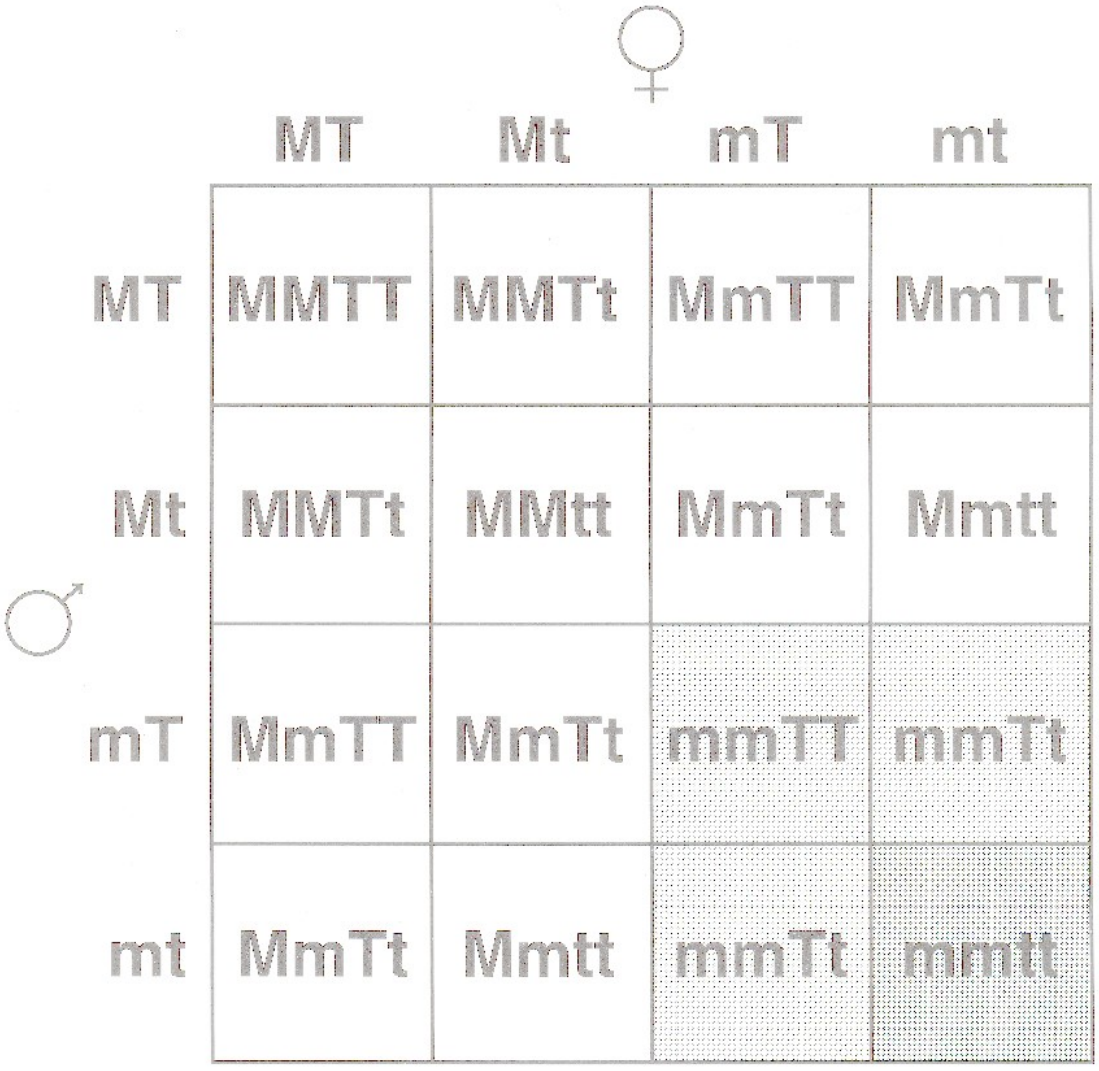
The first order of business is to investigate the genetics of alkaloid production as it exists in plants, especially in the *Phalaris* species.

Festi and Samorini(11) reported 14 alkaloids in *Phalaris arundinacea* and *Phalaris aquatica*. Marum, Hovin and Marten(12) assigned seven of these indole alkaloids to one of three groups, and proposed a genetic model for the production of these groups. Group T contains the tryptamines and carboline derivatives N-methyltryptamine (NMT), N,N-dimethyltryptamine (DMT), and 2-methyl-1,2,3,4-tetrahydro-ß-carboline (MTHC). Group MeO contains the methoxylated tryptamines and carboline derivatives 5-methoxy-N-methyltryptamine(5-MeO-NMT), 5-methoxy-N,N-dimethyltryptamine (5-MEO-DMT), and 2-methyl-6-methoxy-1,2,3,4-tetrahydro-ß-carboline (6-MeO-THC). Group G contains gramine.

According to the Marum model, Group T is controlled by the dominant gene T, and group MeO is controlled by the dominant gene M. The presence of any M masks the effect of T, and Group G is produced only when both genes are homozygous recessive. Thus group G=mmtt, group T=mmT-, and group MeO = M- --.

If we plot out all the possible combinations of M and T, as in Figure Two, we find sixteen possible genetic combinations, of which 12 would yield group MeO alkaloids, 3 would yield group T alkaloids, and only one would yield group G alkaloids. This does not predict the actual percentages of each alkaloid family found in nature, as the frequency of occurrence of each gene in the population is not the same.

Figure 2.
Distribution of M and T genes for alkaloid production in *Phalaris* sp.



M– – – = methoxylated Tryptamines
mmT– = Tryptamines
mmtt = Gramine

A RECENT ALKALOID SURVEY

Fifty-one seed sources of *P. arundinacea* were tested for alkaloid family expression by the author. From 5 to 55 individual seedlings of each seed source were sown in the spring, and the foliage was tested in the fall by the method of Marum *et al* using thin-layer chromatography. Table 1 shows the list of the accessions by plant identification number, their alkaloid ratio, and tentative genetic type.

Eight populations contained the MM homozygous gene for true breeding MeO alkaloid lines. Eight populations contained the homozygous recessive genes for group G. While a few plants tested positive for group T alkaloids, there were no Group T true breeding alkaloid lines, which agrees with Marum et all, who found only 1 % of group T plants in their survey. While there were some Group T plants found, their alkaloid characteristics would be retained only if they would be propagated vegetatively.

Table 1.
Phalaris arundinacea alkaloid family ratios and genotypes.

P I Number	G-M-T Ratio	Population genotype	P I Number	G-M-T Ratio	Population genotype
172443	0-1-0	MM--	369290	1-4-0	Mixed
234694	0-1-0	MM--	435296	1-4-0	Mixed
234697	0-1-0	MM--	435304	1-4-2	Mixed
235547	0-1-0	MM--	435299	11-27-9	Mixed
369291	0-1-0	MM--	435295	12-8-4	Mixed
435305	0-1-0	MM--	315486	15-6-16	Mixed
435308	0-1-0	MM--	255887	17-11-1	Mixed
383726	0-1-0	MM--	392389	2-1-0	Mixed
			435303	2-1-0	Mixed
539029	0-4-1	MmTT	337718	25-26-2	Mixed
			253317	3-14-0	Mixed
227670	1-0-0	mmt	234780	3-2-0	Mixed
422031	1-0-0	mmt	236525	3-2-0	Mixed
435301	1-0-0	mmt	435311	3-2-0	Mixed
435302	1-0-0	mmt	435312	3-2-0	Mixed
435309	1-0-0	mmt	435294	35-18-2	Mixed
440585	1-0-0	mmt	237724	4-2-0	Mixed
557461	1-0-0	mmt	NSL 108391	4-3-0	Mixed
NSL 180170	1-0-0	mmt	539030	5-1-0	Mixed
			253315	5-11-0	Mixed
284179	1-0-1	Mixed	435297	5-29-1	Mixed
235484	1-24-1	Mixed	209979	50-50-0	Mixed
241065	1-1-0	Mixed	505892	6-1-0	Mixed
251531	1-1-0	Mixed	235023	6-11-0	Mixed
315487	1-14-1	Mixed	440584	6-3-0	Mixed
505893	1-2-0	Mixed	422030	6-4-1	Mixed
253316	1-4-0	Mixed	406316	8-8-4	Mixed

ALKALOID BIOSYNTHESIS IN ORGANISMS

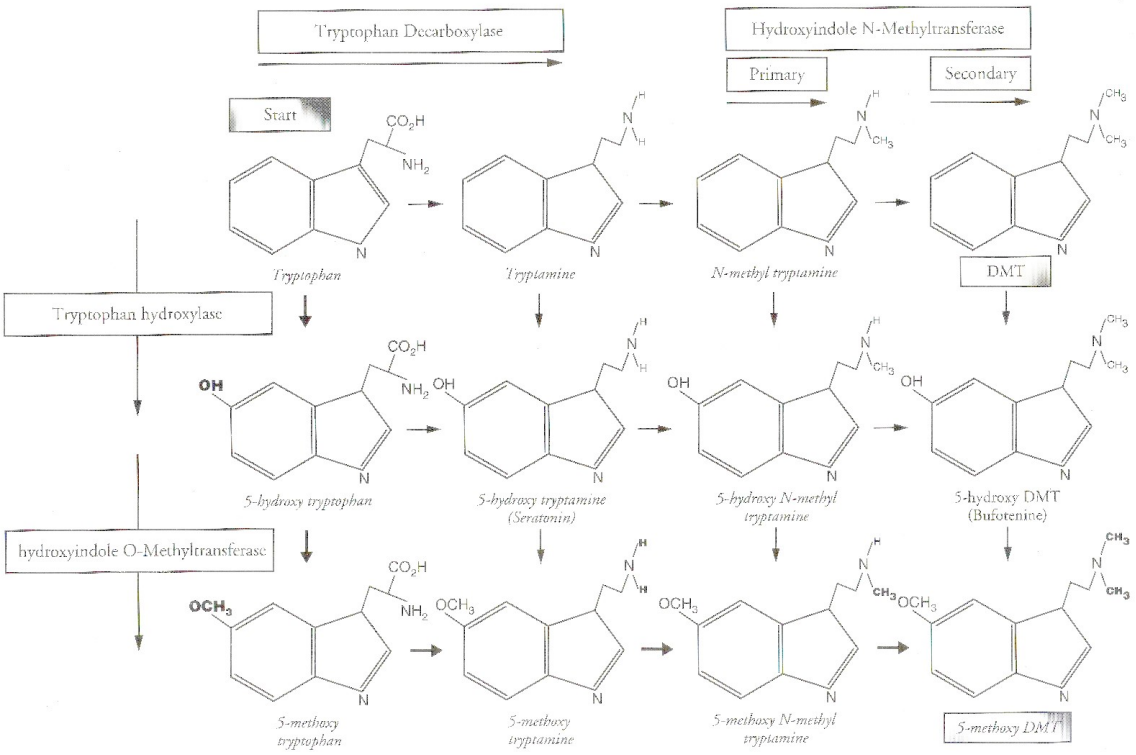
One could next ask the question, what is the biosynthetic pathway which produces DMT and 5-MeO-DMT, and how does it relate to these proposed genetic models?

The biosynthesis chart developed by Baxter and Slaytor(13), and which forms the basis of most of the assumptions in this paper, is shown in Figure three. It starts in the upper left hand corner with tryptophan, one of the twenty essential amino acids which are only obtainable in the diet for mammals.

Each step to the right horizontally, or down vertically, is one enzymatically mediated chemical reaction, with the enzyme responsible for catalyzing that reaction shown in a box. Thus, the first step horizontally shows tryptophan being converted to tryptamine, with the loss of the CO2 group (carboxylase), and the enzyme responsible for catalyzing that reaction being “Tryptophan Decarboxylase”.

Similarly, from tryptophan, one could move vertically down the chart to 5-hydroxy tryptophan by adding a hydroxy (OH) to the 5 position, by the action of the enzyme “Tryptophan hydroxylase.”

Figure 3.
Tryptamine alkaloid Biosynthesis Chart



As one can see, going from tryptophan to DMT involves three enzymatically controlled steps. Going from tryptophan to 5MeO-DMT involves five steps, but which steps is not clear. One needs to look at what route plants actually use to synthesize 5-MeO-DMT.

Marum et al, proposed that the major pathway for 5-MeO DMT production in *P arundinacea* would go directly downward from tryptophan to 5-methoxy tryptophan (presumably going through the 5-hydroxy tryptophan stage), and then progress along the bottom of the chart through the 5-methoxy tryptamine, 5-methoxy N-methyl tryptamine, and 5-methoxy DMT stages.

Baxter and Slator, who did extensive radioactive labeling work on the biosynthesis of these same alkaloids in *P. tuberosa(=aquatica)* reached somewhat ambiguous results, as seven of the alkaloids which were fed as radioactively labeled precursors resulted in the formation of radioactive 5-MeO DMT. One definite result was that DMT was not a precursor for 5-MeO DMT. Their conclusion however, was that the major pathway was as Marum indicated, with alternative pathways

possible. Others have reported that the two N-methyltransferases are different enzymes(14), and that the N-methyltransferases involved in gramine synthesis are different from those involved in tryptamine synthesis(15). As to which gene location corresponds to which enzyme, all that one can say at this point is that perhaps M corresponds with tryptophan hydroxylase, as any M masks T would be consistent with the fact that once tryptophan is hydroxylated, it can no longer become DMT.

Thus to synthesize 5-MeO-DMT in an organism requires the presence of the initial substrate tryptophan (along with other necessary co-factors), and the presence of five enzymes which catalyze the necessary reactions.

As we have seen before, the function of a gene is to code for the production of enzymes. Thus, we are now at the stage of looking for the five genes which code for the production of these five enzymes.

GENETIC SEQUENCES NECESSARY TO CODE FOR THESE ENZYMES

In looking at the first enzyme, tryptophan hydroxylase, four organisms were discovered in which this enzyme has been sequenced, that is, the specific amino acids sequences which comprise this complex protein have been identified(16). In none of the organisms were the amino acid sequences identical, although in each case they catalyzed the identical reaction. This is because an enzyme is a long protein that folds up into a complex three-dimensional structure, and the active catalytic site is only one portion of its surface structure. That surface structure has a specific shape into which the target substrate fits in order to be more easily chemically changed.

Thus the gene that codes for this enzyme will also vary among the various organisms, even though the function that the enzyme will perform will be identical.

However, in looking at the amino acid sequences for these enzymes, one finds portions of the sequences that are identical. Some of these are probably the ‘active site’ sequences that are the same in all species. They are also the sequences that we can use to search for the gene site in an organism that has not been sequenced, such as *Phalaris arundinacea.*

So for example in looking at the sequence codes for the enzyme tryptophan hydroxylase in the organisms human, mouse, rabbit, and rat, we find a sequence of amino acids (using the one letter amino acid codes, Table 3) which is FSQEIGLA in all 4 of these organisms. The equivalent genetic codes are TTC TCC CAA GAA ATT GGC CTG GCT. These are the same in all four organisms, even though many of the amino acids can be coded for by more than one set of three nucleotides.

Table 2 contains some common amino acid sequences and the equivalent genetic codes for 3 of the 5 enzymes required for biosynthesis of 5-MeO-DMT.

Table 2.
Consensus Amino Acid and Nucleotide Sequences for Selected Enzymes.

TRYPTOPHAN HYDROXYLASE								
Amino Acid Sequences	F	S	Q	E	I	G	L	A
Nucleotides:								
Human, Mouse, Rabbit, Rat	TTC	TCC	CAA	GAA	ATT	GGC	CTG	GCT

TRYPTOPHAN DECARBOXYLASE							
Amino Acid Sequences	G	K	E	M	V	D	Y
Nucleotides:							
Human	GGG	AAG	GAG	ATG	GTG	GAT	TAC
Cow	GGG	AAG	GAG	ATG	GTG	GAT	TAC
Rat	GGG	AAG	GAG	ATG	GTG	GAT	TAT

HYDROXYINDOLE O-METHYLTRANSFERASE								
Amino Acid Sequences	D	A	V	R	E	G	R	N
Nucleotides:								
Human	GAC	GCC	GTG	AGA	GAA	GGA	AGG	AAC
Chicken	GAT	GCT	GTG	AGA	GAA	GGA	AGA	AAT

Table 3.
The Genetic Codes.

UUU F Phe	UCU S Ser	UAU Y Tyr	UGU C Cys
UUC F Phe	UCC S Ser	UAC Y Tyr	UGC C Cys
UUA L Leu	UCA S Ser	UAA END	UGA END
UUG L Leu	UCG S Ser	UAG END	UGG W Trp
CUU L Leu	CCU P Pro	CAU H His	CGU R Arg
CUC L Leu	CCC P Pro	CAC H His	CGC R Arg
CUA L Leu	CCA P Pro	CAA Q Gln	CGA R Arg
CUG L Leu	CCG P Pro	CAG Q Gln	CGG R Arg
AUU I Ile	ACU T Thr	AAU N Asn	AGU S Ser
AUC I Ile	ACC T Thr	AAC N Asn	AGC S Ser
AUA I Ile	ACA T Thr	AAA K Lys	AGA R Arg
AUG +M MET	ACG T Thr	AAG K Lys	AGG R Arg
GUU V Val	GCU A Ala	GAU D Asp	GGU G Gly
GUC V Val	GCC A Ala	GAC D Asp	GGC G Gly
GUA V Val	GCA A Ala	GAA E Glu	GGA G Gly
GUG V Val	GCG A Ala	GAG E Glu	GGG G Gly

T = U

GENETIC ENGINEERING WITH AMINO ACID CODES.

It is one thing to know the theoretical codes of a plant product of interest, but is quite another to grapple with the intricacies of actually attempting to find, extract, and insert appropriate gene fragments into other organisms.

In the following section, we will discuss three general approaches to finding and isolating the genetic fragments we are interested in.(17) The three approaches are: 1. Screening of fragmented DNA with a probe, 2. Comparing fragmented DNA patterns of populations to their alkaloid production patterns, and 3. Shotgun cloning. These are very simple conceptual discussions, the actual

techniques require considerable experience and research.

SCREENING FRAGMENTED DNA

In this strategy, DNA is extracted from the plant material and purified. It is then digested or 'fragmented' by the addition of 'restriction enzymes', specialized enzymes that cut strands of DNA at specific points(18,19). This mixture of DNA fragments is then separated by size through a technique called 'gel electrophoresis'(20), which is something like thin-layer chromatography, only in this case the DNA fragments are moved differentially through a gel by an electric current.

This produces a pattern of bands of DNA fragments, each band of which is a different length. One of these bands contains the gene segment we are interested in, but which one? We find the band containing the fragment of interest through a technique called probing. This is a technique that is based on the phenomenon of hybridization. This means that if a segment of DNA is complementary to another segment, it will bond to it, or hybridize with it. Thus if our target strand of DNA has the nucleotide sequence AGCCT for example, the complementary strand to that, TCGGA, would line up and bond with it.

Complementary strands to the gene fragment of interest are called probes. If we know the genetic code for a section of the gene of interest, or, alternatively, if we know the amino acid sequence of the enzyme we are looking for, then we can construct synthetically a section of nucleotides which can serve as a probe. This probe will then attach to the band of gene fragments which has a complementary sequence.

If we also label our probe, through florescent or radioactive methods, then after hybridization, we can use an appropriate visualization technique to determine just which band contains the gene sequence of interest.

One problem with only knowing the amino acid sequence of the enzyme we are looking for is the problem of degeneracy. Degeneracy means that each amino acid can be coded for by more than one set of codons. For example, the amino acid glutamine is coded for by the codons CAA and CAG. Thus in this approach it is necessary to use a population of mixed codons.

Once we have identified a band that has hybridized with our probe, we can remove that band, further cut and electrophorese, until we get down to the specific band of interest. The coding information in Table 2 can be useful in an approach of this sort. Since the most common probes contain 18-30 nucleotides, these sequences should suffice.(21)

2. COMPARING FRAGMENTED DNA PATTERNS OF POPULATIONS TO THEIR ALKALOID PRODUCTION PATTERNS

In this approach, purification of DNA and electrophoresis are also used. However,

in this case, the pattern of bands produced is compared to the known characteristics of the organism, in this case, alkaloid production patterns. Thus, a number of plants would be plated out on one gel, and their fragments separated into bands. Then the patterns of the bands would be compared to each other, as in the now famous 'DNA fingerprinting'(22) Any band that would differ among the group of plants in the same ratio as their alkaloid production characteristics, could be assumed to have a gene for these alkaloid production characteristics in that band.

Thus, in plating out populations of *P. arundinacea* from Table 1, we could plate out ten plants that produce gramine (and have genetic types mmtt), and ten plants that produce methoxylated tryptamines (and have genetic types M---). If we should be so lucky as to get a pattern in which all of the first ten plants differ in one band from all of the second ten plants, than we can perhaps assume that a gene fragment that codes for the production of the alkaloid represented by M resides on that band. This band could then be removed, amplified, further cut and electrophoresed to get down to the specific fragment we are interested in. The information on alkaloid ratios produced by various *P. arundinacea* lines in Table 1 many be useful in this approach.

In the past, such an approach would have been unworkable, as any fragmentation of a whole genome would have produced many thousands of bands, and so they would have been unreadable. Now however, new techniques(23) using unbroken DNA's, enzymes that cut DNA at very rare junctures to produce large DNA fragments, and pulsed-field gel electrophoresis which can handle these large fragments, make such an approach perhaps feasible.

3. SHOTGUN CLONING.

In this approach, we do not look for specific gene fragments to introduce into new organisms. Instead, we fragment the DNA as before, and introduce it wholesale into an appropriate organism, probably in this case yeast cells. We then plate these yeast cells out, let them grow, and test the resulting colonies for the presence of the product we are interested in. This approach has been successful in other cases,(24) and would depend in this case on the development of appropriate testing procedures for the presences of each of the enzymes desired in the yeast colonies. If a colony is producing the appropriate gene product, then presumably it has taken the appropriate gene fragment into its own genetic structure, and is expressing it. Since yeast has had its genetic structure very well studied, any new addition should be detectable and recoverable(25).

TRANSFORMATION OF GENE FRAGMENTS INTO NEW ORGANISMS.

Once we have a genetic fragment of interest, the transformation of that fragment into other organisms can be accomplished by several methods. One class of methods used to transfer genes into other organisms is indirect transfer using

‘vectors’ which are other organisms capable of infecting the target organisms and in the process transferring their genetic information, along with our genetic fragment, into that organism. Examples of this approach are the use of viruses to transfer genes into bacteria, and the use of *Agrobacterium tumefaciens*, or crown gall bacterium to transfer genes into some species of plants during its normal infectious behavior. (26)

The other class of transformation methods is direct gene transfer(24). Some of these are macro and micro-injection, in which DNA is directly injected either into the space surrounding the developing zygote, or directly into the nucleus of a cell. The shotgun approach uses tungsten microprojectiles adsorbed with DNA projected by an explosive charge into cells. In the whiskers method, cells are added to a liquid along with DNA and microscopic particles with a needle-like shape such as silicon carbide crystals. In chemically mediated DNA uptake, the cell wall of the target organism is dissolved chemically so that DNA can enter the cell directly . Electroporation has also been used, in which electrical discharge is employed to create temporary pores in the cell wall.

Once inside the cell, the genetic engineer faces another host of problems in trying to detect which of the target cells have successfully taken up the new genetic material, whether the expression of the genetic instructions require other co-factors or substrates, and whether the genetic constituents will be passed on to other subsequent generations without becoming selected against.

In furthering the availability of vision plant compounds, the best choice of a target organism would probably be a yeast. If successful, a strain of yeast with stable genes for the production of vision plant compounds could be dried, transported, rehydrated, and grown anywhere with only the necessity of the addition of the original substrate, in this case tryptophan, a substance found in such foods as peanuts and sesame seeds.

THE FUTURE OF EVOLUTION

One can see that the future of evolution, heretofore a three billion year process of chance mutation and painful evolutionary selection, from this point on will be one of deliberate choice, either by society at large, or, more likely, certain individuals or groups within it.

Our future evolution will involve self-directed evolution of our states of consciousness, as well as our physiology. It has been said that in many cases the evolution of life forms proceeds by the prolongation of the juvenal form of a species. For example, human most closely resemble the juvenal form of the apes. Similarly, future humans may most closely resemble our juvenal form, which includes a more active pineal gland.

Each new leap of evolutionary development must be viewed with trepidation by those involved. This is a very extraordinary proposal. I submit that a clear-eyed

view of our present course of development must call for extraordinary proposals.

The vision of those who have tasted the unity experience afforded by the ingestion of 5-MeO DMT will, I believe, give great impetus to the genetic development outlined above. A small, committed group could produce startling results in a matter of years. Once the full implications of the possibilities are grasped, one becomes committed to working toward the communication and implementation of this vision.

Those whose only experience with the tryptamines is with DMT, either smokable or in ayahuasca formulations, may perhaps be taken aback by the thought of being in this state full time. However, those who have used 5-MeO DMT in low doses in oral ayahuasca analog mixtures will know that this state can be one of calm connection and profound awareness.

We now know how to take a gene out of anything, and put it into anything, even ourselves. We can, for better or worse, take control of our own evolution, genetically engineering ourselves into whatever self-image the collective unconscious has been striving for. Our response to the information streaming into the collective unconscious in the form of biodynamically mediated molecules, is to reach toward that source of information, and to strive to integrate ourselves more fully with it. This we do at present in very primitive form.

However, the time is coming when we can integrate the light-filled DNA sequences from the vision plants into our own bodies. We have the means at hand to transform the genetic codes for psychobotanical substances into organisms such as *E. coli*, which have an on-going symbiotic relationship with us in our gut. More than that, we have the means to transform our own genetic structures, as well as other advanced life forms on this planet, such as dolphins.

What this implies for the future in terms of evolutionary possibilities is in line, I believe, with the invitation of the realm of light. There is an ongoing evolutionary tendency at work at every level of the universe to form elements into larger and more inclusive wholes called holons(27). A holon composed of a group of elementary particles would be a stable atom. A holon composed of human beings would be a group mind or group being. The experiencing of group energy fields and group minds while temporarily under the influence of the neurotransmitter 5-MeO DMT, leads one to imagine that the future holon that our race may become could include this vitamin supplementation as a part of our normal development. Biological evolution is indeed at a unique point in its journey.

> “I saw that the sacred hoop of my people was one of many hoops that made one circle, and in the center grew one mighty flowering tree to shelter all the children of one mother and one father. And I saw that it was holy. Beneath it all the animals were mingling with the people like relatives and making happy cries”
>
> BLACK ELK

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